

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2006, 20:58:58 ; Search time 200 Seconds
(without alignments)
720.377 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccctatagtgagaaca.....aactttaaatgcatgggtaa 77

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 18

Total number of hits satisfying chosen parameters: 211

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
		Query					
Result	No.	Score	Match	Length	DB	ID	Description
	1	77	100.0	840	2	US-07-979-966A-1	Sequence 1, Appli
	2	77	100.0	845	2	US-08-589-446-3	Sequence 3, Appli
	3	77	100.0	845	2	US-08-444-882-3	Sequence 3, Appli
	4	77	100.0	845	2	US-08-389-459A-3	Sequence 3, Appli
	5	77	100.0	845	3	US-08-987-867A-3	Sequence 3, Appli
	6	77	100.0	1314	3	US-08-392-794A-1	Sequence 1, Appli
	7	77	100.0	2095	2	US-08-333-901-5	Sequence 5, Appli

EW

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OM nucleic - nucleic search, using sw model

Run on: June 11, 2006, 20:50:48 ; Search time 695 Seconds
(without alignments)
772.465 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccctatagtcgagaaca.....aactttaaatgcatgggtaa 77

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 18

Total number of hits satisfying chosen parameters: 491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	77	100.0	566	1	AAN71252	Aan71252 Sequence
2	77	100.0	630	6	ABK14492	Abk14492 Alpha Gal